

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Ullrich, Axel
Gishizsky, Mikhail
Sures, Irman G.

(ii) TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine Kinases

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pennie & Edmonds
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/426,509
(B) FILING DATE: 21-APR-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/282,545
(B) FILING DATE: 22-APR-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7683-074

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-9741
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

A

CTCGCTCCAA	GTTGTG	CAGC	CGGGACCGCC	TCGGGGTGTG	CAGCCGGCTC	GCGGAGGCCC	60
TCCTGGGGGC	GGGCGCGGGG	CGGCTCGGGG	GCGCCCCCTG	AGCAGAAAAC	AGGAAGAACC		120
AGGCTCGGTC	CAGTGGCACC	CAGCTCCCTA	CCTCCTGTGC	CAGCCGCCTG	GCCTGTGGCA		180
GGCCATTCCC	AGCGTCCCCG	ACTGTGACCA	CTTGCTCAGT	GTGCCTCTCA	CCTGCCTCAG		240
TTTCCCTCTG	GGGGGCGATG	GCGGGGCGAG	GCTCTCTGGT	TTCCTGGCGG	GCATTTACG		300
GCTGTGATTC	TGCTGAGGAA	CTTCCCCGGG	TGAGCCCCCG	CTTCCTCCGA	GCCTGGCACC		360
CCCCTCCCGT	CTCAGCCAGG	ATGCCAACGA	GGCGCTGGGC	CCCGGGCACC	CAGTGTATCA		420
CCAAATGCGA	GCACACCCGC	CCCAAGCCAG	GGGAGCTGGC	CTTCCGCAAG	GGCGACGTGG		480
TCACCATCCT	GGAGGCCTGC	GAGAAACAAGA	GCTGGTACCG	CGTCAAGCAC	CACACCAGTG		540
GACAGGAGGG	GCTGCTGGCA	GCTGGGCGCG	TGCGGGAGCG	GGAGGCCCTC	TCCGCAGACC		600
CCAAGCTCAG	CCTCATGCCG	TGGTTCCACG	GGAAGATCTC	GGGCCAGGAG	GCTGTCCAGC		660
AGCTGCAGCC	TCCCGAGGAT	GGGCTGTTCC	TGGTGCGGGA	GTCCGCGCGC	CACCCCGGCG		720
ACTACGTCCT	GTGCGTGAGC	TTTGGCCGCG	ACGTCATCCA	CTACCGCGTG	CTGCACCGCG		780
ACGGCCACCT	CACAATCGAT	GAGGCCGTGT	TCTTCTGCAA	CCTCATGGAC	ATGGTGGAGC		840
ATTACAGCAA	GGACAAGGGC	GCTATCTGCA	CCAAGCTGGT	GAGACCAAAG	CGGAAACACG		900
GGACCAAGTC	GGCCGAGGAG	GAGCTGGCCA	GGGCGGGCTG	GTTACTGAAC	CTGCAGCATT		960
TGACATTGGG	AGCACAGATC	GGAGAGGGAG	AGTTTGGAGC	TGTCCTGCAG	GGTGAGTACC		1020
TGGGGCAAAA	GGTGGCCGTG	AAGAATATCA	AGTGTGATGT	GACAGCCCAG	GCCTTCCTGG		1080
ACGAGACGGC	CGTCATGACG	AAGATGCAAC	ACGAGAACCT	GGTGCCTCTC	CTGGGCGTGA		1140
TCCTGCACCA	GGGGCTGTAC	ATTGTCATGG	AGCACGTGAG	CAAGGGCAAC	CTGGTGAACT		1200
TTCTGCGGAC	CCGGGGTCGA	GCCCTCGTGA	ACACCGCTCA	GCTCCTGCAG	TTTTCTCTGC		1260
ACGTGGCCGA	GGGCATGGAG	TACCTGGAGA	GCAAGAAGCT	TGTGCACCGC	GACCTGGCCG		1320
CCCGCAACAT	CCTGGTCTCA	GAGGACCTGG	TGGCCAAGGT	CAGCGACTTT	GGCCTGGCCA		1380
AAGCCGAGCG	GAAGGGGCTA	GACTCAAGCC	GGCTGCCCCG	CAAGTGGACG	GCGCCCGAGG		1440
CTCTCAAACA	CGGGAAGTTC	ACCAGCAAGT	CGGATGTCTG	GAGTTTTGGG	GTGCTGCTCT		1500
GGGAGGTCTT	CTCATATGGA	CGGGCTCCGT	ACCCTAAAAT	GTCACTGAAA	GAGGTGTCCG		1560
AGGCCGTGGA	GAAGGGGTAC	CGCATGGAAC	CCCCCGAGGG	CTGTCCAGGC	CCCGTGCACG		1620
TCCTCATGAG	CAGCTGCTGG	GAGGCAGAGC	CCGCCC GCCG	GCCACCCTTC	CGCAAACCTGG		1680
CCGAGAAGCT	GGCCCGGGAG	CTACGCAGTG	CAGGTGCCCC	AGCCTCCGTC	TCAGGGCAGG		1740
ACGCCGACGG	CTCCACCTCG	CCCCGAAGCC	AGGAGCCCTG	ACCCACCCCG	GTGGGGCCCT		1800
TGGCCCCAGA	GGACCGAGAG	AGTGGAGAGT	GCGGCGTGGG	GGCACTGACC	AGGCCCAAGG		1860
AGGGTCCAGG	CGGGCAAGTC	ATCCTCCTGG	TGCCACAGC	AGGGGCTGGC	CCACGTAGGG		1920

A

GGCTCTGGGC GGCCCGTGGA CACCCCAGAC CTGCGAAGGA TGATCGCCCG ATAAAGACGG 1980
ATTCTAAGGA CTCTAAAAAA 2000

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg Ala Phe His Gly Cys
1 5 10 15
Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro Arg Phe Leu Arg Ala
20 25 30
Trp His Pro Pro Pro Val Ser Ala Arg Met Pro Thr Arg Arg Trp Ala
35 40 45
Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His Thr Arg Pro Lys Pro
50 55 60
Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val Thr Ile Leu Glu Ala
65 70 75 80
Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His His Thr Ser Gly Gln
85 90 95
Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu Arg Glu Ala Leu Ser
100 105 110
Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Ser
115 120 125
Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro Glu Asp Gly Leu Phe
130 135 140
Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp Tyr Val Leu Cys Val
145 150 155 160
Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val Leu His Arg Asp Gly
165 170 175
His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys Asn Leu Met Asp Met
180 185 190
Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile Cys Thr Lys Leu Val
195 200 205
Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
210 215 220
Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
225 230 235 240

7A

Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
245 250 255
Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
260 265 270
Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
275 280 285
Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
290 295 300
Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
305 310 315 320
Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
325 330 335
Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
340 345 350
Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
355 360 365
Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
370 375 380
Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
385 390 395 400
Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
405 410 415
Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
420 425 430
Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
435 440 445
Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
450 455 460
Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
465 470 475 480
Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala
485 490 495
Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
500 505

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTTTTGG	CTTAGAGCTT	GAGAGTCAAA	GTTAAGGACC	CACATGTATA	CTTCGGCTCT	60
AGCGAGTCTA	AGGATGATAA	TATGGATACA	AAATCTATTC	TAGAAGAACT	TCTTCTCAAA	120
AGATCACAGC	AAAAGAAGAA	AATGTCACCA	AATAATTACA	AAGAACGGCT	TTTTGTTTTG	180
ACCAAAACAA	ACCTTTCCTA	CTATGAATAT	GACAAAATGA	AAAGGGGCAG	CAGAAAAGGA	240
TCCATTGAAA	TTAAGAAAAT	CAGATGTGTG	GAGAAAGTAA	ATCTCGAGGA	GCAGACGCCT	300
GTAGAGAGAC	AGTACCCATT	TCAGATTGTC	TATAAAGATG	GGCTTCTCTA	TGTCTATGCA	360
TCAAATGAAG	AGAGCCGAAG	TCAGTGGTTG	AAAGCATTAC	AAAAAGAGAT	AAGGGGTAAC	420
CCCCACCTGC	TGGTCAAGTA	CCATAGTGGG	TTCTTCGTGG	ACGGGAAGTT	CCTGTGTTGC	480
CAGCAGAGCT	GTAAAGCAGC	CCCAGGATGT	ACCCTCTGGG	AAGCATATGC	TAATCTGCAT	540
ACTGCAGTCA	ATGAAGAGAA	ACACAGAGTT	CCCACCTTCC	CAGACAGAGT	GCTGAAGATA	600
CCTCGGGCAG	TTCCTGTTCT	CAAAATGGAT	GCACCATCTT	CAAGTACCAC	TCTAGCCCAA	660
TATGACAACG	AATCAAAGAA	AACTATGGC	TCCCAGCCAC	CATCTTCAAG	TACCAGTCTA	720
GCGCAATATG	ACAGCAACTC	AAAGAAAATC	TATGGCTCCC	AGCCAAACTT	CAACATGCAG	780
TATATTCCAA	GGGAAGACTT	CCCTGACTGG	TGGCAAGTAA	GAAAACTGAA	AAGTAGCAGC	840
AGCAGTGAAG	ATGTTGCAAG	CAGTAACCAA	AAAGAAAGAA	ATGTGAATCA	CACCACCTCA	900
AAGATTTTCAT	GGGAATTCCC	TGAGTCAAGT	TCATCTGAAG	AAGAGGAAAA	CCTGGATGAT	960
TATGACTGGT	TTGCTGGTAA	CATCTCCAGA	TCACAATCTG	AACAGTTACT	CAGACAAAAG	1020
GGAAAAGAAG	GAGCATTTAT	GGTTAGAAAT	TCGAGCCAAG	TGGGAATGTA	CACAGTGTCC	1080
TTATTTAGTA	AGGCTGTGAA	TGATAAAAAA	GGAAGTGTCA	AACATTACCA	CGTGCATACA	1140
AATGCTGAGA	ACAAATTATA	CCTGGCAGAA	AACTACTGTT	TTGATTCCAT	TCCAAAGCTT	1200
ATTCATTATC	ATCAACACAA	TTCAGCAGGC	ATGATCACAC	GGCTCCGCCA	CCCTGTGTCA	1260
ACAAAGGCCA	ACAAGGTCCC	CGACTCTGTG	TCCCTGGGAA	ATGGAATCTG	GGAAGTGAAG	1320
AGAGAAGAGA	TTACCTTGTT	GAAGGAGCTG	GGAAGTGGCC	AGTTTGGAGT	GGTCCAGCTG	1380
GGCAAGTGGA	AGGGGCAGTA	TGATGTTGCT	GTTAAGATGA	TCAAGGAGGG	CTCCATGTCA	1440
GAAGATGAAT	TCTTTCAGGA	GGCCCAGACT	ATGATGAAAC	TCAGCCATCC	CAAGCTGGTT	1500
AAATTCTATG	GAGTGTGTTC	AAAGGAATAC	CCCATATACA	TAGTGACTGA	ATATATAAGC	1560
AATGGCTGCT	TGCTGAATTA	CCTGAGGAGT	CACGGAAAAG	GACTTGAACC	TTCCCAGCTC	1620
TTAGAAATGT	GCTACGATGT	CTGTGAAGGC	ATGGCCTTCT	TGGAGAGTCA	CCAATTCATA	1680
CACCGGGACT	TGGCTGCTCG	TAACTGCTTG	GTGGACAGAG	ATCTCTGTGT	GAAAGTATCT	1740
GACTTTGGAA	TGACAAGGTA	TGTTCTTGAT	GACCAGTATG	TCAGTTCAGT	CGGAACAAAG	1800
TTTCCAGTCA	AGTGGTCAGC	TCCAGAGGTG	TTTCATTACT	TCAAATACAG	CAGCAAGTCA	1860

10

GACGTATGGG CATTGTTGGAT CCTGATGTGG GAGGTGTTCA GCCTGGGGAA GCAGCCCTAT 1920
GACTTGTATG ACAACTCCCA GGTGGTTCTG AAGGTCTCCC AGGGCCACAG GCTTTACCGG 1980
CCCCACCTGG CATCGGACAC CATCTACCAG ATCATGTACA GCTGCTGGCA CGAGCTTCCA 2040
GAAAAGCGTC CCACATTTCA GCAACTCCTG TCTTCCATTG AACCACTTCG GGAAAAAGAC 2100
AAGCATTGAA GAAGAAATTA GGAGTGCTGA TAAGAATGAA TATAGATGCT GGCCAGCATT 2160
TTCATTCAATT TTAAGGAAAG TAGCAAGGCA TAATGTAATT TAGCTAGTTT TTAATAGTGT 2220
TCTCTGTATT GTCTATTATT TAGAAATGAA CAAGGCAGGA AACAAAAGAT TCCCTTGAAA 2280
TTTAGGTCAA ATTAGTAATT TTGTTTATGC TGCCCCTGAT ATAACACTTT CCAGCCTATA 2340
GCAGAAGCAC ATTTTCAGAC TGCAATATAG AGACTGTGTT CATGTGTAAA GACTGAGCAG 2400
AACTGAAAAA TTAATTATTG GATATTCATT CTTTCTTTA TATTGTCATT GTCACAACAA 2460
TTAAATATAC TACCAAGTAC AAAAAAAAAA AAAAAAAAAA 2500

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Thr Lys Ser Ile Leu Glu Glu Leu Leu Leu Lys Arg Ser Gln
1 5 10 15
Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr Lys Glu Arg Leu Phe Val
20 25 30
Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu Tyr Asp Lys Met Lys Arg
35 40 45
Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
50 55 60
Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
65 70 75 80
Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
85 90 95
Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly
100 105 110
Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
115 120 125
Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr
130 135 140

A

Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys
145 150 155 160
His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
165 170 175
Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala
180 185 190
Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser
195 200 205
Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr
210 215 220
Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
225 230 235 240
Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Ser Glu
245 250 255
Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
260 265 270
Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Ser Glu Glu Glu
275 280 285
Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser
290 295 300
Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met
305 310 315 320
Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
325 330 335
Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
340 345 350
Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
355 360 365
Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
370 375 380
Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro
385 390 395 400
Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
405 410 415
Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
420 425 430
Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys
435 440 445
Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met
450 455 460
Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
465 470 475 480

Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
485 490 495

Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
500 505 510

Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
515 520 525

Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
530 535 540

Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr
545 550 555 560

Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
565 570 575

Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
580 585 590

Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
595 600 605

Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
610 615 620

Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
625 630 635 640

Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
645 650 655

Pro Thr Phe Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys
660 665 670

Asp Lys His
675

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGACTGGT CGAAAGACAG GAACAGACTT GAAACAGGGG GAGAGCTCCT GCGGAAACGA 60

AGACGTGGAG GTTTTACCAG GGATAAGAAG AAAAGACACC TTCCTAGTGA GCACTGCCC 120

AGCTCCTGCT CAGTTTGTCC TCGGGGTAGC ACCTCCAGCC ACAGAAAGCA AGCCGGTAAG 180

TCTCTCCAGG TAGGACTTGC TGCAACCCAG CTGCTGGACT GATCTGAAAC GGGACTTTGC 240

ATACTCTCCG AAGTATGGTG AGTTGGTGCT GACTTCAAAG TTGCCTGGTG AAGGAAGATA 300

A

AGGTGGATCG	CAGAGACTAA	GGGGAGAGGG	AGAAGCCCTG	CTCCTCTTCT	CCCCACCAAG	360
GCACAATGAG	CAACATCTGT	CAGAGGCTCT	GGGAGTACCT	AGAACCCTAT	CTCCCCTGTT	420
TGTCCACGGA	GGCAGACAAG	TCAACCGTGA	TTGAAAATCC	AGGGGCCCTT	TGCTCTCCCC	480
AGTCACAGAG	GCATGGCCAC	TACTTTGTGG	CTTTGTTTGA	TTACCAGGCT	CGGACTGCTG	540
AGGACTTGAG	CTTCCGAGCA	GGTGACAAAC	TTCAAGTTCT	GGACACTTTG	CATGAGGGCT	600
GGTGGTTTGC	CAGACACTTG	GAGAAAAGAC	GAGATGGCTC	CAGTCAGCAA	CTACAAGGCT	660
ATATTCCTTC	TAACTACGTG	GCTGAGGACA	GAAGCCTACA	GGCAGAGCCG	TGGTTCTTTG	720
GAGCAATCGG	AAGATCAGAT	GCAGAGAAAC	AACTATTATA	TTCAGAAAAC	AAGACCGGTT	780
CCTTTCTAAT	CAGAGAAAGT	GAAAGCCAAA	AAGGAGAATT	CTCTCTTTCA	GTTTTAGATG	840
GAGCAGTTGT	AAAACACTAC	AGAATTAAAA	GACTGGATGA	AGGGGGATTT	TTTCTCACGC	900
GAAGAAGAAT	CTTTTCAACA	CTGAACGAAT	TTGTGAGCCA	CTACACCAAG	ACAAGTGACG	960
GCCTGTGTGT	CAAGCTGGGG	AAACCATGCT	TAAAGATCCA	GGTCCCAGCT	CCATTTGATT	1020
TGTCGTATAA	AACCGTGGAC	CAATGGGAGA	TAGACCGCAA	CTCCATACAG	CTTCTGAAGC	1080
GATTGGGATC	TGGTCAGTTT	GGCGAAGTAT	GGGAGGTCT	GTGGAACAAT	ACCACTCCAG	1140
TAGCAGTGAA	AACATTAAAA	CCAGGTTCAA	TGGATC AAA	TGACTTCCTG	AGGGAGGCAC	1200
AGATAATGAA	GAACCTAAGA	CATCCAAAGC	TTATCCAGCT	TTATGCTGTT	TGCACTTTAG	1260
AAGATCCAAT	TTATATTATT	ACAGAGTTGA	TGAGACATGG	AAGTCTGCAA	GAATATCTCC	1320
AAAATGACAC	TGGATCAAAA	ATCCATCTGA	CTCAACAGGT	AGACATGGCG	GCACAGGTTG	1380
CCTCTGGAAT	GGCCTATCTG	GAGTCTCGGA	ACTACATTCA	CAGAGATCTG	GCTGCCAGAA	1440
ATGTCCTCGT	TGGTGAACAT	AATATCTACA	AAGTAGCAGA	TTTTGGACTT	GCCAGAGTTT	1500
TTAAGGTAGA	TAATGAAGAC	ATCTATGAAT	CTAGACACGA	AATAAAGCTG	CCGGTGAAGT	1560
GGACTGCGCC	CGAAGCCATT	CGTAGTAATA	AATTCAGCAT	TAAGTCCGAT	GTATGGTCAT	1620
TTGGAATCCT	TCTTTATGAA	ATCATTACTT	ATGGCAAAAT	GCCTTACAGT	GGTATGACAG	1680
GTGCCCAGGT	AATCCAGATG	TTGGCTCAAA	ACTATAGACT	TCCGCAACCA	TCCAAGTGTG	1740
CACAGCAATT	TTACAACATC	ATGTTGGAGT	GCTGGAATGC	AGAGCCTAAG	GAACGACCTA	1800
CATTTGAGAC	ACTGCGTTGG	AAACTTGAAG	ACTATTTTGA	AACAGACTCT	TCATATTTCAG	1860
ATGCAAATAA	CTTCATAAGA	TGAACACTGG	AGAAGAATAT	CAAATAATAA	AGTAGCAAAA	1920
CAAATTCAAA	TAATCCATTG	CAAAATACAA	TGTTATCAAC	CAACTGCACA	ATCAGTTTAT	1980
CCTGACATAT	TCAAGTGATA	GGATAAAGTT	GGCCATGTAT	TATGAAAAAG	ATTATTTGTG	2040
CATTTTATTG	ACTGGGCAAC	ACTGCAGGAC	AGTCAAGGTC	ATATATAATT	GCTCACTGCC	2100
TGGAAAATTA	AGCACACTAA	ACCAAGTTAT	TTTTCTTTTT	AAGAGATACT	TACATTTCCA	2160
TTTATTGTTT	GAAATGTCGC	GATCAAGAGA	ATCAACAGAT	GATAGTCCAA	TTTTTACTCA	2220

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GTGATGACTG TGTAGCATTTC TCCTGTTTAC TGATTAGAGT GGTTATTCAT TATTCCTCAG 2280
ATTGCTGAAT CCCATCAGGC TGTTATTATG AAGGAATTTG ATTGCTTTGC TGCACAGCAG 2340
GACCTGTGCT TTGAGATTTT TTTTCTCTT TTAAAATATC CTGTAACCTAC AATGATGGTA 2400
AAGCCATGTT AAATGACTTG ATTGTACTTG GAGTAATTGC ACATTTTTTT CTATGCATAA 2460
AAAAATGATG CAGCTGTTGA GAAAACGAAG TCTTTTTCAT TTTGCAGAAG GAAATGATGG 2520
AATTTTTCTG TACTTCAGTA TGTGTCAACT GAGAGTCATA TACATTAGTT TTAATCTCTT 2580
AATATTGAGA ATCAGGTTGC AAAACGGATG AGTTATTATC TATGGAAATG TGAGAAATGT 2640
CTAATAGCCC ATAAAGTCTG AGAAATAGGT ATCAAATAG TTTAGGAAAA TGAGAGGAGA 2700
ACAGTAGGAT TGCTGTGGCC TAGACTTCTG AGTAATTAAT AAAGAAAAAG AAGTACCAA 2760
AAAAAAAAAA 2770

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Ser Trp Cys Met Ser Asn Ile Cys Gln Arg Leu Trp Glu Tyr
1 5 10 15
Leu Glu Pro Tyr Leu Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr
20 25 30
Val Ile Glu Asn Pro Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His
35 40 45
Gly His Tyr Phe Val Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu
50 55 60
Asp Leu Ser Phe Arg Ala Gly Asp Lys Lys Leu Gln Val Leu Asp Thr
65 70 75 80
Leu His Glu Gly Trp Trp Phe Ala Arg His Leu Glu Lys Arg Arg Asp
85 90 95
Gly Ser Ser Gln Gln Leu Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala
100 105 110
Glu Asp Arg Ser Leu Gln Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly
115 120 125
Arg Ser Asp Ala Glu Lys Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly
130 135 140
Ser Phe Leu Ile Arg Glu Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu
145 150 155 160

A

Ser Val Leu Asp Gly Ala Val Val Lys His Tyr Arg Ile Lys Arg Leu
165 170 175

Asp Glu Gly Gly Phe Phe Leu Thr Arg Arg Arg Ile Phe Ser Thr Leu
180 185 190

Asn Glu Phe Val Ser His Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val
195 200 205

Lys Leu Gly Lys Pro Cys Leu Lys Ile Gln Val Pro Ala Pro Phe Asp
210 215 220

Leu Ser Tyr Lys Thr Val Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile
225 230 235 240

Gln Leu Leu Lys Arg Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Glu
245 250 255

Gly Leu Trp Asn Asn Thr Thr Pro Val Ala Val Lys Thr Leu Lys Pro
260 265 270

Gly Ser Met Asp Pro Asn Asp Phe Leu Arg Glu Ala Gln Ile Met Lys
275 280 285

Asn Leu Arg His Pro Lys Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu
290 295 300

Glu Asp Pro Ile Tyr Ile Ile Thr Glu Leu Met Arg His Gly Ser Leu
305 310 315 320

Gln Glu Tyr Leu Gln Asn Asp Thr Gly Ser Lys Ile His Leu Thr Gln
325 330 335

Gln Tyr Asp Met Ala Ala Gln Val Ala Ser Gly Met Ala Tyr Leu Glu
340 345 350

Ser Arg Asn Tyr Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
355 360 365

Gly Glu His Asn Ile Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val
370 375 380

Phe Lys Val Asp Asn Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys
385 390 395 400

Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe
405 410 415

Ser Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile
420 425 430

Ile Thr Tyr Gly Lys Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val
435 440 445

Ile Gln Met Leu Ala Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys
450 455 460

Pro Gln Gln Phe Tyr Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro
465 470 475 480

Lys Glu Arg Pro Thr Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr
485 490 495

A

Phe Glu Thr Asp Ser Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg
500 505 510

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Ala	Ile	Gln	Ala	Ala	Trp	Pro	Ser	Gly	Thr	Glu	Cys	Ile	Ala	1	5	10	15
Lys	Tyr	Asn	Phe	His	Gly	Thr	Ala	Glu	Gln	Asp	Leu	Pro	Phe	Cys	Lys	20	25	30	
Gly	Asp	Val	Leu	Thr	Ile	Val	Ala	Val	Thr	Lys	Asp	Pro	Asn	Trp	Tyr	35	40	45	
Lys	Ala	Lys	Asn	Lys	Val	Gly	Arg	Glu	Gly	Ile	Ile	Pro	Ala	Asn	Tyr	50	55	60	
Val	Gln	Lys	Arg	Glu	Gly	Val	Lys	Ala	Gly	Thr	Lys	Leu	Ser	Leu	Met	65	70	75	80
Pro	Trp	Phe	His	Gly	Lys	Ile	Thr	Arg	Glu	Gln	Ala	Glu	Arg	Leu	Leu	85	90	95	
Tyr	Pro	Pro	Glu	Thr	Gly	Leu	Phe	Leu	Val	Arg	Glu	Ser	Thr	Asn	Tyr	100	105	110	
Pro	Gly	Asp	Tyr	Thr	Leu	Cys	Val	Ser	Cys	Asp	Gly	Lys	Val	Glu	His	115	120	125	
Tyr	Arg	Ile	Met	Tyr	His	Ala	Ser	Lys	Leu	Ser	Ile	Asp	Glu	Glu	Val	130	135	140	
Tyr	Phe	Glu	Asn	Leu	Met	Gln	Leu	Val	Glu	His	Tyr	Thr	Ser	Asp	Ala	145	150	155	160
Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ile	Lys	Pro	Lys	Val	Met	Glu	Gly	Thr	165	170	175	
Val	Ala	Ala	Gln	Asp	Glu	Phe	Tyr	Arg	Ser	Gly	Trp	Ala	Leu	Asn	Met	180	185	190	
Lys	Glu	Leu	Lys	Leu	Leu	Gln	Thr	Ile	Gly	Lys	Gly	Glu	Phe	Gly	Asp	195	200	205	
Val	Met	Leu	Gly	Asp	Tyr	Arg	Gly	Asn	Lys	Val	Ala	Val	Lys	Cys	Ile	210	215	220	
Lys	Asn	Asp	Ala	Thr	Ala	Gln	Ala	Phe	Leu	Ala	Glu	Ala	Ser	Val	Met	225	230	235	240

18

Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
 245 250 255
 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
 260 265 270
 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
 275 280 285
 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
 290 295 300
 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
 305 310 315 320
 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
 325 330 335
 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
 340 345 350
 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
 355 360 365
 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
 370 375 380
 Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
 385 390 395 400
 Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
 405 410 415
 Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
 420 425 430
 Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
 435 440 445
 His Leu
 450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
 1 5 10 15
 Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
 20 25 30

A

Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
35 40 45
Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
50 55 60
Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
65 70 75 80
Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
85 90 95
Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
100 105 110
Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
115 120 125
Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
130 135 140
Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
145 150 155 160
Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
165 170 175
Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
180 185 190
Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
195 200 205
Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
210 215 220
Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
225 230 235 240
Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
245 250 255
Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
260 265 270
Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
275 280 285
Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
290 295 300
Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
305 310 315 320
Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
325 330 335
Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
340 345 350
Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
355 360 365

A

Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
370 375 380
Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
385 390 395 400
Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
405 410 415
Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
420 425 430
Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
435 440 445
Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
450 455 460
Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
465 470 475 480
Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
485 490 495
Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
500 505 510
Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
515 520 525
Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
530 535 540
Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
545 550 555 560
Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
565 570 575
Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
580 585 590
Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
595 600 605
His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
610 615 620
Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
625 630 635 640
Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
645 650 655
Glu Glu Ser

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown

A

(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Asn	Asn	Phe	Ile	Leu	Leu	Glu	Glu	Gln	Leu	Ile	Lys	Lys	Ser	Gln
1				5					10					15	
Gln	Lys	Arg	Arg	Thr	Ser	Pro	Ser	Asn	Phe	Lys	Val	Arg	Phe	Phe	Val
			20					25					30		
Leu	Thr	Lys	Ala	Ser	Leu	Ala	Tyr	Phe	Glu	Asp	Arg	His	Gly	Lys	Lys
		35					40					45			
Arg	Thr	Leu	Lys	Gly	Ser	Ile	Glu	Leu	Ser	Arg	Ile	Lys	Cys	Val	Glu
	50					55					60				
Ile	Val	Lys	Ser	Asp	Ile	Ser	Ile	Pro	Cys	His	Tyr	Lys	Tyr	Pro	Phe
65					70					75					80
Gln	Val	Val	His	Asp	Asn	Tyr	Leu	Leu	Tyr	Val	Phe	Ala	Pro	Asp	Arg
				85					90					95	
Glu	Ser	Arg	Gln	Arg	Trp	Val	Leu	Ala	Leu	Lys	Glu	Glu	Thr	Arg	Asn
			100					105					110		
Asn	Asn	Ser	Leu	Val	Pro	Lys	Tyr	His	Pro	Asn	Phe	Trp	Met	Asp	Gly
		115					120					125			
Lys	Trp	Arg	Cys	Cys	Ser	Gln	Leu	Glu	Lys	Leu	Ala	Thr	Gly	Cys	Ala
	130					135					140				
Gln	Tyr	Asp	Pro	Thr	Lys	Asn	Ala	Ser	Lys	Lys	Pro	Leu	Pro	Pro	Thr
145					150					155					160
Pro	Glu	Asp	Asn	Arg	Arg	Pro	Leu	Trp	Glu	Pro	Glu	Glu	Thr	Val	Val
				165					170					175	
Ile	Ala	Leu	Tyr	Asp	Tyr	Gln	Thr	Asn	Asp	Pro	Gln	Glu	Leu	Ala	Leu
			180					185					190		
Arg	Arg	Asn	Glu	Glu	Tyr	Cys	Leu	Leu	Asp	Ser	Ser	Glu	Ile	His	Trp
		195					200					205			
Trp	Arg	Val	Gln	Asp	Arg	Asn	Gly	His	Glu	Gly	Tyr	Val	Pro	Ser	Ser
	210					215					220				
Tyr	Leu	Val	Glu	Lys	Ser	Pro	Asn	Asn	Leu	Glu	Thr	Tyr	Glu	Trp	Tyr
225					230					235					240
Asn	Lys	Ser	Ile	Ser	Arg	Asp	Lys	Ala	Glu	Lys	Leu	Leu	Leu	Asp	Thr
				245					250					255	
Gly	Lys	Glu	Gly	Ala	Phe	Met	Val	Arg	Asp	Ser	Arg	Thr	Ala	Gly	Thr
			260					265					270		
Tyr	Thr	Val	Ser	Val	Phe	Thr	Lys	Ala	Val	Val	Ser	Glu	Asn	Asn	Pro
		275					280					285			
Cys	Ile	Lys	His	Tyr	His	Ile	Lys	Glu	Thr	Asn	Asp	Asn	Pro	Lys	Arg

A

290					295					300					
Tyr	Tyr	Val	Ala	Glu	Lys	Tyr	Val	Phe	Asp	Ser	Ile	Pro	Leu	Leu	Ile
305					310					315					320
Asn	Tyr	His	Gln	His	Asn	Gly	Gly	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr
				325					330					335	
Pro	Val	Cys	Phe	Gly	Arg	Gln	Lys	Ala	Pro	Val	Thr	Ala	Gly	Leu	Arg
			340					345					350		
Tyr	Gly	Lys	Trp	Val	Ile	Asp	Pro	Ser	Glu	Leu	Thr	Phe	Val	Gln	Glu
		355					360					365			
Ile	Gly	Ser	Gly	Gln	Phe	Gly	Leu	Val	His	Leu	Gly	Tyr	Trp	Leu	Asn
	370					375					380				
Lys	Asp	Lys	Val	Ala	Ile	Lys	Thr	Ile	Arg	Glu	Gly	Ala	Met	Ser	Glu
385					390					395					400
Glu	Asp	Phe	Ile	Glu	Glu	Ala	Glu	Val	Met	Met	Lys	Leu	Ser	His	Pro
				405					410					415	
Lys	Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys	Leu	Glu	Gln	Ala	Pro	Ile	Cys
			420					425					430		
Leu	Val	Phe	Glu	Phe	Met	Glu	His	Gly	Cys	Leu	Ser	Asp	Tyr	Leu	Arg
		435					440					445			
Thr	Gln	Arg	Gly	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Leu	Gly	Met	Cys	Leu
	450					455					460				
Asp	Val	Cys	Glu	Gly	Met	Ala	Tyr	Leu	Glu	Glu	Ala	Cys	Val	Ile	His
465					470					475					480
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Gln	Val	Ile
				485					490					495	
Lys	Val	Ser	Asp	Phe	Gly	Met	Thr	Arg	Phe	Val	Leu	Asp	Asp	Gln	Tyr
			500					505					510		
Thr	Ser	Ser	Thr	Gly	Thr	Lys	Phe	Pro	Val	Lys	Trp	Ala	Ser	Pro	Glu
			515				520					525			
Val	Phe	Ser	Phe	Ser	Arg	Tyr	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe
	530					535					540				
Gly	Val	Leu	Met	Trp	Glu	Val	Phe	Ser	Glu	Gly	Lys	Ile	Pro	Tyr	Glu
545					550					555					560
Asn	Arg	Ser	Asn	Ser	Glu	Val	Val	Glu	Asp	Ile	Ser	Thr	Gly	Phe	Arg
				565					570					575	
Leu	Tyr	Lys	Pro	Arg	Leu	Ala	Ser	Thr	His	Val	Tyr	Gln	Ile	Met	Asn
			580					585					590		
His	Cys	Trp	Lys	Glu	Arg	Pro	Glu	Asp	Arg	Pro	Ala	Phe	Ser	Arg	Leu
			595				600					605			
Leu	Arg	Gln	Leu	Ala	Glu	Ile	Ala	Glu	Ser	Gly	Leu				
	610					615					620				

(2) INFORMATION FOR SEQ ID NO:10:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Met	Val	Ser	Phe	Pro	Val	Lys	Ile	Asn	Phe	His	Ser	Ser	Pro	Gln
1				5					10					15	
Ser	Arg	Asp	Arg	Trp	Val	Lys	Lys	Leu	Lys	Glu	Glu	Ile	Lys	Asn	Asn
			20					25					30		
Asn	Asn	Ile	Met	Ile	Lys	Tyr	His	Pro	Lys	Phe	Trp	Ala	Asp	Gly	Ser
		35					40					45			
Tyr	Gln	Cys	Cys	Arg	Gln	Thr	Glu	Lys	Leu	Ala	Pro	Gly	Cys	Glu	Lys
	50					55					60				
Tyr	Asn	Leu	Phe	Glu	Ser	Ser	Ile	Arg	Lys	Thr	Leu	Pro	Pro	Ala	Pro
65					70					75					80
Glu	Ile	Lys	Lys	Arg	Arg	Pro	Pro	Pro	Pro	Ile	Pro	Pro	Glu	Glu	Glu
				85				90						95	
Asn	Thr	Glu	Glu	Ile	Val	Val	Ala	Met	Tyr	Asp	Phe	Gln	Ala	Thr	Glu
			100					105					110		
Ala	His	Asp	Leu	Arg	Leu	Glu	Arg	Gly	Gln	Glu	Tyr	Ile	Ile	Leu	Glu
		115					120					125			
Lys	Asn	Asp	Leu	His	Trp	Trp	Arg	Ala	Arg	Asp	Lys	Tyr	Gly	Trp	Tyr
	130					135					140				
Cys	Arg	Asn	Thr	Asn	Arg	Ser	Lys	Ala	Glu	Gln	Leu	Leu	Arg	Thr	Glu
145					150					155					160
Asp	Lys	Glu	Gly	Gly	Phe	Met	Val	Arg	Asp	Ser	Ser	Gln	Pro	Gly	Leu
				165					170					175	
Tyr	Thr	Val	Ser	Leu	Tyr	Thr	Lys	Phe	Gly	Gly	Glu	Gly	Ser	Ser	Gly
			180					185					190		
Phe	Arg	His	Tyr	His	Ile	Lys	Glu	Thr	Ala	Thr	Ser	Pro	Lys	Lys	Tyr
		195					200					205			
Tyr	Leu	Ala	Glu	Lys	His	Ala	Phe	Gly	Ser	Ile	Pro	Glu	Ile	Ile	Glu
	210					215					220				
Tyr	His	Lys	His	Asn	Ala	Ala	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr	Pro
225					230					235					240
Val	Ser	Thr	Lys	Gly	Lys	Asn	Ala	Pro	Thr	Thr	Ala	Gly	Phe	Ser	Tyr
				245					250					255	
Asp	Lys	Trp	Glu	Ile	Asn	Pro	Ser	Glu	Leu	Thr	Phe	Met	Arg	Glu	Leu
			260					265					270		

Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln
275 280 285
Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu
290 295 300
Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys
305 310 315 320
Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile
325 330 335
Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln
340 345 350
Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp
355 360 365
Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg
370 375 380
Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys
385 390 395 400
Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr
405 410 415
Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val
420 425 430
Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly
435 440 445
Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys
450 455 460
Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu
465 470 475 480
His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg
485 490 495
Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu
500 505 510
Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg
515 520 525

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Gly	Cys	Val	Gln	Cys	Lys	Asp	Lys	Glu	Ala	Thr	Lys	Leu	Thr	Glu
1				5					10					15	
Glu	Arg	Asp	Gly	Ser	Leu	Asn	Gln	Ser	Ser	Gly	Tyr	Arg	Tyr	Gly	Thr
			20					25					30		
Asp	Pro	Thr	Pro	Gln	His	Tyr	Pro	Ser	Phe	Gly	Val	Thr	Ser	Ile	Pro
		35					40					45			
Asn	Tyr	Asn	Asn	Phe	His	Ala	Ala	Gly	Gly	Gln	Gly	Leu	Thr	Val	Phe
	50					55					60				
Gly	Gly	Val	Asn	Ser	Ser	Ser	His	Thr	Gly	Thr	Leu	Arg	Thr	Arg	Gly
65					70				75						80
Gly	Thr	Gly	Val	Thr	Leu	Phe	Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg
				85					90					95	
Thr	Glu	Asp	Asp	Leu	Ser	Phe	His	Lys	Gly	Glu	Lys	Phe	Gln	Ile	Leu
			100					105					110		
Asn	Ser	Ser	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Thr	Thr	Gly
		115					120					125			
Glu	Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile
	130					135					140				
Gln	Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Leu	Gly	Arg	Lys	Asp	Ala	Glu
145					150					155					160
Arg	Gln	Leu	Leu	Ser	Phe	Gly	Asn	Pro	Arg	Gly	Thr	Phe	Leu	Ile	Arg
				165					170					175	
Glu	Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp
			180					185					190		
Asp	Asp	Met	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu
		195					200					205			
Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Glu	Thr	Leu
	210					215					220				
Gln	Gln	Leu	Val	Gln	His	Tyr	Ser	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys
225					230					235					240
Arg	Leu	Val	Val	Pro	Cys	His	Lys	Gly	Met	Pro	Arg	Leu	Thr	Asp	Leu
				245					250					255	
Ser	Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln
			260					265					270		
Leu	Ile	Lys	Arg	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly
		275					280					285			
Thr	Trp	Asn	Gly	Asn	Thr	Lys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly
	290					295					300				
Thr	Met	Ser	Pro	Glu	Ser	Phe	Leu	Glu	Glu	Ala	Gln	Ile	Met	Lys	Lys
305					310					315					320

A

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
325 330 335

Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30

8

Asp	Pro	Thr	Gln	Leu	Ser	Gly	Ala	Phe	Thr	His	Ile	Pro	Asp	Phe	Asn
	35						40					45			
Asn	Phe	His	Ala	Ala	Ala	Val	Ser	Pro	Pro	Val	Pro	Phe	Ser	Gly	Pro
	50					55					60				
Gly	Phe	Tyr	Pro	Cys	Asn	Thr	Leu	Gln	Ala	His	Ser	Ser	Ile	Thr	Gly
65					70					75					80
Gly	Gly	Val	Thr	Leu	Phe	Ile	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr
				85					90					95	
Glu	Asp	Asp	Leu	Ser	Phe	Gln	Lys	Gly	Glu	Lys	Phe	His	Ile	Ile	Asn
			100					105					110		
Asn	Thr	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Ala
		115					120					125			
Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln
	130					135					140				
Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg
145					150					155					160
Gln	Leu	Leu	Cys	His	Gly	Asn	Cys	Arg	Gly	Thr	Phe	Leu	Ile	Arg	Glu
				165					170					175	
Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp
			180					185					190		
Glu	Ala	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp
		195					200					205			
Ser	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Ile	Gln
	210					215					220				
Gln	Leu	Val	Gln	His	Tyr	Ile	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys	Arg
225					230					235					240
Leu	Ala	Val	Pro	Cys	Pro	Lys	Gly	Thr	Pro	Lys	Leu	Ala	Asp	Leu	Ser
				245					250					255	
Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln	Leu
			260					265					270		
Leu	Gln	Lys	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr
	275					280						285			
Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr
	290					295					300				
Met	Ser	Pro	Glu	Ala	Phe	Leu	Glu	Glu	Ala	Gln	Ile	Met	Lys	Arg	Leu
305					310					315					320
Arg	His	Asp	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro
				325					330					335	
Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser	Gln	Gly	Ser	Leu	Leu	Asp	Phe
			340					345					350		
Leu	Lys	Asp	Gly	Asp	Gly	Arg	Tyr	Leu	Lys	Leu	Pro	Gln	Leu	Val	Asp
		355					360					365			

18

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln
530 535

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80

8

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
85 90 95
Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
100 105 110
Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
115 120 125
Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
130 135 140
Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
145 150 155 160
Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
165 170 175
Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
180 185 190
Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
195 200 205
Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
210 215 220
Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
225 230 235 240
Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
245 250 255
Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
260 265 270
Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
275 280 285
Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
290 295 300
Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
305 310 315 320
Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
325 330 335
Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
340 345 350
Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
355 360 365
Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
370 375 380
Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
385 390 395 400
Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
420 425 430
Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
435 440 445
Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
450 455 460
Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
465 470 475 480
Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
485 490 495
Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510
Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
515 520 525
Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
1 5 10 15
Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
20 25 30
Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ala Lys
35 40 45
Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
50 55 60
Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
65 70 75 80
Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
85 90 95
Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
100 105 110
Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
115 120 125
Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser

8

130						135									140
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe
145					150					155					160
Gly	Lys	Met	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Leu	Leu	Leu	Asn	Pro	Gly
				165					170					175	
Asn	Gln	Arg	Gly	Ile	Phe	Leu	Val	Arg	Glu	Ser	Glu	Thr	Thr	Lys	Gly
			180					185					190		
Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Glu	Ile	Arg	Gly	Asp	Asn
		195					200					205			
Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Asn	Gly	Gly	Tyr	Tyr	Ile
	210					215					220				
Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Leu	Gln	Lys	Leu	Val	Lys	His	Tyr
225					230					235					240
Thr	Glu	His	Ala	Asp	Gly	Leu	Cys	His	Lys	Leu	Thr	Thr	Val	Cys	Pro
				245					250					255	
Thr	Val	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile
			260				265						270		
Pro	Arg	Glu	Ser	Leu	Arg	Leu	Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe
		275					280					285			
Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Ile
	290					295					300				
Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Met	Pro	Glu	Ala	Phe	Leu	Gln	Glu
305					310					315					320
Ala	Gln	Ile	Met	Lys	Lys	Leu	Arg	His	Asp	Lys	Leu	Val	Pro	Leu	Tyr
				325					330					335	
Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser
			340					345					350		
Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Glu	Gly	Asp	Gly	Lys	Tyr	Leu
		355					360					365			
Lys	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Ile	Ala	Asp	Gly	Met
	370					375					380				
Ala	Tyr	Ile	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala
385					390					395					400
Asn	Ile	Leu	Val	Gly	Glu	Asn	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly
				405					410					415	
Leu	Ala	Arg	Leu	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala
			420					425					430		
Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg
		435					440					445			
Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Gln	Thr	Glu
450						455					460				

8

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
165 170 175

18

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe
325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
500 505 510

18

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln
515 520 525

Thr

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
1 5 10 15
Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30
Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
35 40 45
Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
50 55 60
Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
65 70 75 80
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
100 105 110
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125
Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
130 135 140
Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
145 150 155 160
Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175
Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
180 185 190
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
195 200 205
Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
210 215 220

Ala	Cys	Ile	Ser	Pro	Lys	Pro	Gln	Lys	Pro	Trp	Asp	Lys	Asp	Ala	Trp
225					230					235					240
Glu	Ile	Pro	Arg	Glu	Ser	Ile	Lys	Leu	Val	Lys	Arg	Leu	Gly	Ala	Gly
				245					250					255	
Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Asn	Ser	Thr	Lys	Val
			260					265					270		
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Val	Gln	Ala	Phe	Leu
		275					280					285			
Glu	Glu	Ala	Asn	Leu	Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Arg
	290					295					300				
Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu
305					310					315					320
Tyr	Met	Ala	Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly
				325					330					335	
Gly	Lys	Val	Leu	Leu	Pro	Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala
			340					345					350		
Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Lys	Asn	Tyr	Ile	His	Arg	Asp	Leu
		355					360					365			
Arg	Ala	Ala	Asn	Val	Leu	Val	Ser	Glu	Ser	Leu	Met	Cys	Lys	Ile	Ala
	370					375					380				
Asp	Phe	Gly	Leu	Ala	Arg	Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg
385					390					395					400
Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn
				405					410					415	
Phe	Gly	Cys	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu
			420					425					430		
Leu	Tyr	Glu	Ile	Val	Thr	Tyr	Gly	Lys	Ile	Pro	Tyr	Pro	Gly	Arg	Thr
		435					440					445			
Asn	Ala	Asp	Val	Met	Thr	Ala	Leu	Ser	Gln	Gly	Tyr	Arg	Met	Pro	Arg
	450					455					460				
Val	Glu	Asn	Cys	Pro	Asp	Glu	Leu	Tyr	Asp	Ile	Met	Lys	Met	Cys	Trp
465					470					475					480
Lys	Glu	Lys	Ala	Glu	Glu	Arg	Pro	Thr	Phe	Asp	Tyr	Leu	Gln	Ser	Val
				485					490					495	
Leu	Asp	Asp	Phe	Tyr	Thr	Ala	Thr	Glu	Gly	Gln	Tyr	Gln	Gln	Gln	Pro
			500					505					510		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

A

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Ser	Met	Lys	Ser	Lys	Phe	Leu	Gln	Val	Gly	Gly	Asn	Thr	Phe	
1				5					10					15		
Ser	Lys	Thr	Glu	Thr	Ser	Ala	Ser	Pro	His	Cys	Pro	Val	Tyr	Val	Pro	
			20					25					30			
Asp	Pro	Thr	Ser	Thr	Ile	Lys	Pro	Gly	Pro	Asn	Ser	His	Asn	Ser	Asn	
			35				40					45				
Thr	Pro	Gly	Ile	Arg	Glu	Ala	Gly	Ser	Glu	Asp	Ile	Ile	Val	Val	Ala	
	50					55					60					
Leu	Tyr	Asp	Tyr	Glu	Ala	Ile	His	His	Glu	Asp	Leu	Ser	Phe	Gln	Lys	
65					70					75					80	
Gly	Asp	Gln	Met	Val	Val	Leu	Glu	Glu	Ser	Gly	Glu	Trp	Trp	Lys	Ala	
				85					90					95		
Arg	Ser	Leu	Ala	Thr	Arg	Lys	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	
			100					105					110			
Ala	Arg	Val	Asp	Ser	Leu	Glu	Thr	Glu	Glu	Trp	Phe	Phe	Lys	Gly	Ile	
		115					120					125				
Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	Gly	Asn	Met	Leu	
	130					135					140					
Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys	Gly	Ser	Tyr	Ser	
145					150					155					160	
Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	Asp	Thr	Val	Lys	His	
				165					170					175		
Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	Ile	Ser	Pro	Arg	
			180					185					190			
Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	His	Tyr	Lys	Lys	Gly	
		195					200					205				
Asn	Asp	Gly	Leu	Cys	Gln	Lys	Leu	Ser	Val	Pro	Cys	Met	Ser	Ser	Lys	
	210					215					220					
Pro	Gln	Lys	Pro	Trp	Glu	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	
225					230					235					240	
Leu	Lys	Leu	Glu	Lys	Lys	Leu	Gly	Ala	Gly	Gln	Phe	Gly	Glu	Val	Trp	
				245					250					255		
Met	Ala	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	
			260					265					270			
Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	Val	Met	
		275					280					285				
Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	Val	Thr	
	290					295					300					

8

Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
 305 310 315 320
 Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
 325 330 335
 Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
 340 345 350
 Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365
 Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
 370 375 380
 Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
 385 390 395 400
 Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
 405 410 415
 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
 420 425 430
 Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
 435 440 445
 Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
 450 455 460
 Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
 465 470 475 480
 Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
 485 490 495
 Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 500 505

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
 1 5 10 15
 Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
 20 25 30
 Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45

18

Val	Thr	Tyr	Glu	Gly	Ser	Asn	Pro	Pro	Ala	Ser	Pro	Leu	Gln	Asp	Asn
50						55					60				
Leu	Val	Ile	Ala	Leu	His	Ser	Tyr	Glu	Pro	Ser	His	Asp	Gly	Asp	Leu
65					70					75					80
Gly	Phe	Glu	Lys	Gly	Glu	Gln	Leu	Arg	Ile	Leu	Glu	Gln	Ser	Gly	Glu
				85					90					95	
Trp	Trp	Lys	Ala	Gln	Ser	Leu	Thr	Thr	Gly	Gln	Glu	Gly	Phe	Ile	Pro
			100					105					110		
Phe	Asn	Phe	Val	Ala	Lys	Ala	Asn	Ser	Leu	Glu	Pro	Glu	Pro	Trp	Phe
		115					120					125			
Phe	Lys	Asn	Leu	Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro
	130					135					140				
Gly	Asn	Thr	His	Gly	Ser	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Ser	Thr	Ala
145					150					155					160
Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Gln	Asn	Gln	Gly	Glu
				165					170					175	
Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Asn	Leu	Asp	Asn	Gly	Gly	Phe	Tyr
			180				185						190		
Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Gly	Leu	His	Glu	Leu	Val	Arg	His
		195					200					205			
Tyr	Thr	Asn	Ala	Ser	Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ser	Arg	Pro	Cys
	210					215					220				
Gln	Thr	Gln	Lys	Pro	Gln	Lys	Pro	Trp	Trp	Glu	Asp	Glu	Trp	Glu	Val
225					230					235					240
Pro	Arg	Glu	Thr	Leu	Lys	Leu	Val	Glu	Arg	Leu	Gly	Ala	Gly	Gln	Phe
				245					250					255	
Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Gly	His	Thr	Lys	Val	Ala	Val
			260					265					270		
Lys	Ser	Leu	Lys	Gln	Gly	Ser	Met	Ser	Pro	Asp	Ala	Phe	Leu	Ala	Glu
		275					280					285			
Ala	Asn	Leu	Met	Lys	Gln	Leu	Gln	His	Gln	Arg	Leu	Val	Arg	Leu	Tyr
	290					295					300				
Ala	Val	Val	Thr	Gln	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Met	Glu
305					310					315					320
Asn	Gly	Ser	Leu	Val	Asp	Phe	Leu	Lys	Thr	Pro	Ser	Gly	Ile	Lys	Leu
			325						330					335	
Thr	Ile	Asn	Lys	Leu	Leu	Asp	Met	Ala	Ala	Gln	Ile	Ala	Glu	Gly	Met
			340					345					350		
Ala	Phe	Ile	Glu	Glu	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala
		355					360					365			
Asn	Ile	Leu	Val	Ser	Asp	Thr	Leu	Ser	Cys	Lys	Ile	Ala	Asp	Phe	Gly
	370					375					380				

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
500 505

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 499 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly
1 5 10 15

Trp Ser Pro Val Lys Ile Arg Thr Gln Asp Lys Ala Pro Pro Pro Leu
20 25 30

Pro Pro Leu Val Val Phe Asn His Leu Ala Pro Pro Ser Pro Asn Gln
35 40 45

Asp Pro Asp Glu Glu Glu Arg Phe Val Val Ala Leu Phe Asp Tyr Ala
50 55 60

Ala Val Asn Asp Arg Asp Leu Gln Val Leu Lys Gly Glu Lys Leu Gln
65 70 75 80

Val Leu Arg Ser Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr
85 90 95

Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Pro Val Glu Thr
100 105 110

Leu Glu Val Glu Lys Trp Phe Phe Arg Thr Ile Ser Arg Lys Asp Ala
115 120 125

8

Glu	Arg	Gln	Leu	Leu	Ala	Pro	Met	Asn	Lys	Ala	Gly	Ser	Phe	Leu	Ile
130						135					140				
Arg	Glu	Ser	Glu	Ser	Asn	Lys	Gly	Ala	Phe	Ser	Leu	Ser	Val	Lys	Asp
145					150					155					160
Ile	Thr	Thr	Gln	Gly	Glu	Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Ser	Leu
				165					170					175	
Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Thr	Leu
			180					185					190		
Gln	Ala	Leu	Val	Gln	His	Tyr	Ser	Lys	Lys	Gly	Asp	Gly	Leu	Cys	Gln
		195					200					205			
Lys	Leu	Thr	Leu	Pro	Cys	Val	Asn	Leu	Ala	Pro	Lys	Asn	Leu	Trp	Ala
	210					215					220				
Gln	Asp	Glu	Trp	Glu	Ile	Pro	Arg	Gln	Ser	Leu	Lys	Leu	Val	Arg	Lys
225					230					235					240
Leu	Gly	Ser	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Lys	Asn
				245					250					255	
Asn	Met	Lys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Glu	Gly	Thr	Met	Ser	Pro
			260					265					270		
Glu	Ala	Phe	Leu	Gly	Glu	Ala	Asn	Val	Met	Lys	Thr	Leu	Gln	His	Glu
		275					280					285			
Arg	Leu	Val	Arg	Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Pro	Ile	Tyr	Ile
	290					295					300				
Val	Thr	Glu	Tyr	Met	Ala	Arg	Gly	Cys	Leu	Leu	Asp	Phe	Leu	Lys	Thr
305					310					315					320
Asp	Glu	Gly	Ser	Arg	Leu	Ser	Leu	Pro	Arg	Leu	Ile	Asp	Met	Ser	Ala
				325					330					335	
Gln	Val	Ala	Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Met	Asn	Ser	Ile	His
			340					345					350		
Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val	Ser	Glu	Thr	Leu	Cys	Cys
		355					360					365			
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ile	Asp	Ser	Glu	Tyr	Thr
	370					375					380				
Ala	Gln	Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala
385					390					395					400
Ile	His	Phe	Gly	Val	Phe	Thr	Ile	Lys	Ala	Asp	Val	Trp	Ser	Phe	Gly
				405					410					415	
Val	Leu	Leu	Met	Val	Ile	Val	Thr	Tyr	Gly	Arg	Val	Pro	Tyr	Pro	Gly
			420					425					430		
Met	Ser	Asn	Pro	Glu	Val	Ile	Arg	Ser	Leu	Glu	His	Gly	Tyr	Arg	Met
		435					440					445			
Pro	Cys	Pro	Glu	Thr	Cys	Pro	Pro	Glu	Leu	Tyr	Asn	Asp	Ile	Ile	Thr
	450					455					460				

A

Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu
465 470 475 480

Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu
485 490 495

Leu Gln Pro

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATTCCCA CAGNGACTTN GCNGCNAG

28

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCGA ANGTCANAC GTCNGA

26

*13
cancel.*

X